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Application No: 10569000 Version No: 4.0

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Total Warnings: 1
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No. of SeqIDs Defined: 44
Actual SeqID Count: 44

Error code	Error Description
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SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
Hannah, L. Curtis
Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose
Pyrophosphorylase

<130> UF.371XC1

<140> 10569000

<141> 2011-03-01

<150> PCT/US2004/026965

<151> 2004-08-18

<150> 60/496,188

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<160> 44

<170> PatentIn version 3.5

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Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile		
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Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys		
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Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp			
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Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val		
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Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala		
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Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val		
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Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
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Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
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Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
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Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
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Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
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Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
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Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
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Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
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Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
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Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
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Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
35 40 45

Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
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Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
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Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu

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Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
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Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
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Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
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Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
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Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
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Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
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Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
370 375 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385 390 395 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
405 410 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
420 425 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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Ile Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
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Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65 70 75 80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
85 90 95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
115 120 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
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Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
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Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
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Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
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Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
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Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
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Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
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Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
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Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
370 375 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385 390 395 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
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Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
420